

WHAT IS CLAIMED IS:

1. An isolated polynucleotide from corynebacteria which contains a polynucleotide sequence selected from the group consisting of:
 - a) a polynucleotide which is at least 70% identical to a polynucleotide encoding a polypeptide containing the amino acid sequence of SEQ ID NO: 2,
 - b) a polynucleotide encoding a polypeptide containing an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID NO:2,
 - c) a polynucleotide which is complementary to the polynucleotides of a) or b), and
 - d) a polynucleotide containing at least 15 consecutive bases of the polynucleotide sequence of a), b) or c).
2. The polynucleotide according to Claim 1 which is a DNA replicatable in corynebacteria.
3. The polynucleotide according to Claim 2 that is a recombinant DNA.
4. The polynucleotide according to Claim 1 which is an RNA.
5. The polynucleotide according to Claim 2 containing the nucleic acid sequence as shown in SEQ ID NO:1.

6. Replicable DNA according to Claim 2 containing:

- 5 (i) the nucleotide sequence shown in SEQ ID NO:1,
or
- (ii) at least one sequence corresponding to sequence
(i) within the degeneracy of the genetic code,
or
- 10 (iii) at least one sequence which hybridizes with the
sequence complementary to sequence (i) or (ii),
and optionally
- 15 (iv) neutral sense mutations in (i).

7. The polynucleotide according to Claim 2 encoding a
polypeptide containing the amino acid sequence as
shown in SEQ ID NO:2.

- 20 8. A fermentation process for the preparation of an L-
amino acid, comprising the following steps:
- a) fermentation of the L-lysine-producing
corynebacteria in which at least the gpm gene or
- 25 nucleotide sequences coding therefor are
amplified and, in particular, overexpressed,
- b) enrichment of the L-amino acid in the medium or
in the cells of the bacteria, and
- c) isolation of the L-amino acid.

30 9. The process according to Claim 8 wherein the L-amino
acid is L-lysine.

10. The process according to Claim 8, characterized in that bacteria are used in which other genes of the biosynthetic pathway of the desired L-amino acid are additionally amplified.
- 5 11. The process according to Claim 8, characterized in that bacteria are used in which the metabolic pathways which reduce the formation of L-lysine are at least partially switched off.
- 10 12. The process according to Claim 8, characterized in that a strain transformed with a plasmid vector is used and the plasmid vector carries the nucleotide sequence coding for the gpm gene.
- 15 13. The process according to one of Claims 7 to 10, characterized in that corynebacteria which produce L-lysine are used.
- 20 14. The process according to Claim 10, characterized in that the dapA gene coding for dihydrodipicolinate synthase is simultaneously overexpressed.
- 25 15. The process according to Claim 10, characterized in that a DNA fragment which confers S-(2-aminoethyl)cysteine resistance is simultaneously amplified.
- 30 16. The process according to Claim 10, characterized in that the gap gene coding for glyceraldehyde 3-phosphate dehydrogenase is simultaneously overexpressed.

17. The process according to Claim 10, characterized in that the *tpi* gene coding for triose phosphate isomerase is simultaneously overexpressed.
- 5 18. The process according to Claim 10, characterized in that the *pgk* gene coding for 3-phosphoglycerate kinase is simultaneously overexpressed.
- 10 19. The process according to Claim 10, characterized in that the *pyc* gene coding for pyruvate carboxylase is simultaneously overexpressed.
- 15 20. A process for the production of DNA of genes which develop an action corresponding to the *opcA* gene comprising employment of the polynucleotide sequences according to Claim 1 as primers in a polymerase chain reaction.
- 20 21. A hybridization probe comprising a polynucleotide sequence according to claim 1.
- 25 22. Coryneform microorganisms transformed by the introduction of the replicatable DNA according to one of Claims 1 or 6.
23. Microorganisms according to claim 22 from the genus *Corynebacterium*.